

Fig 1

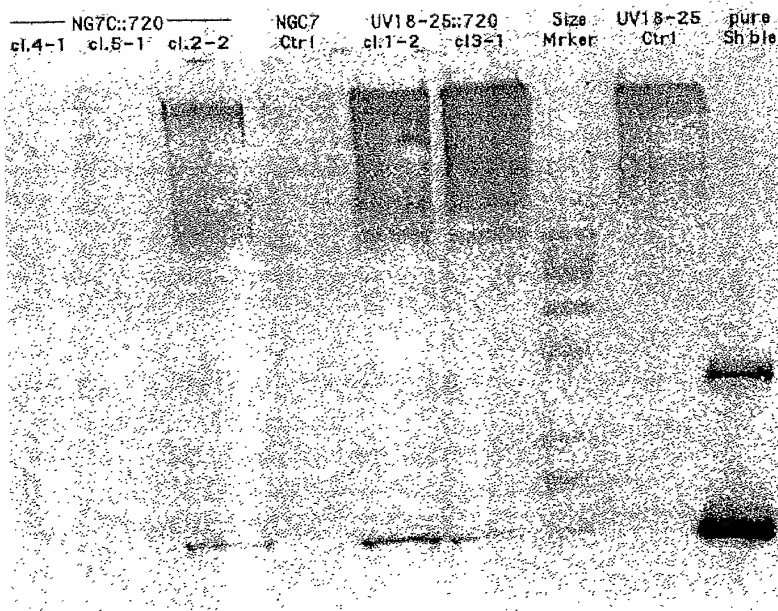


Fig 2

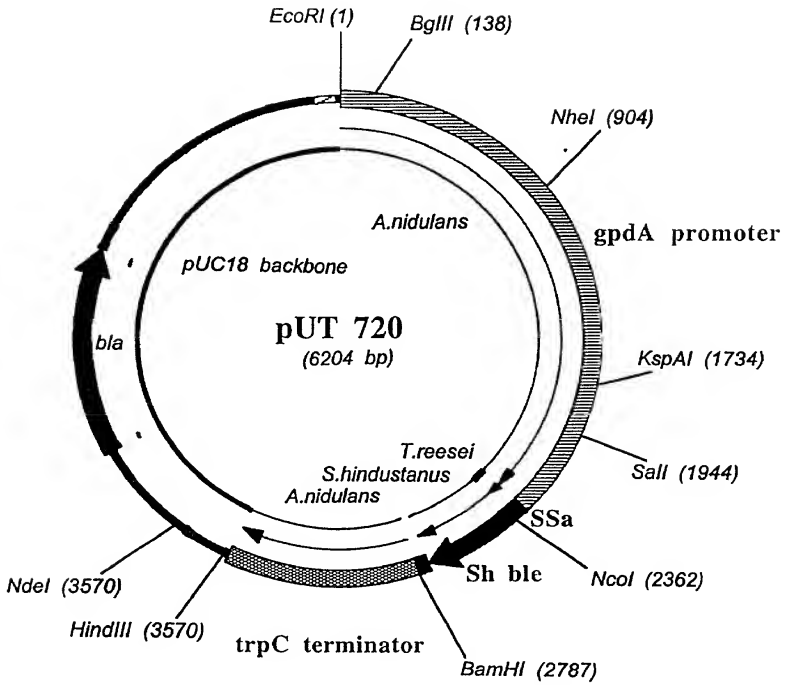


Fig 3

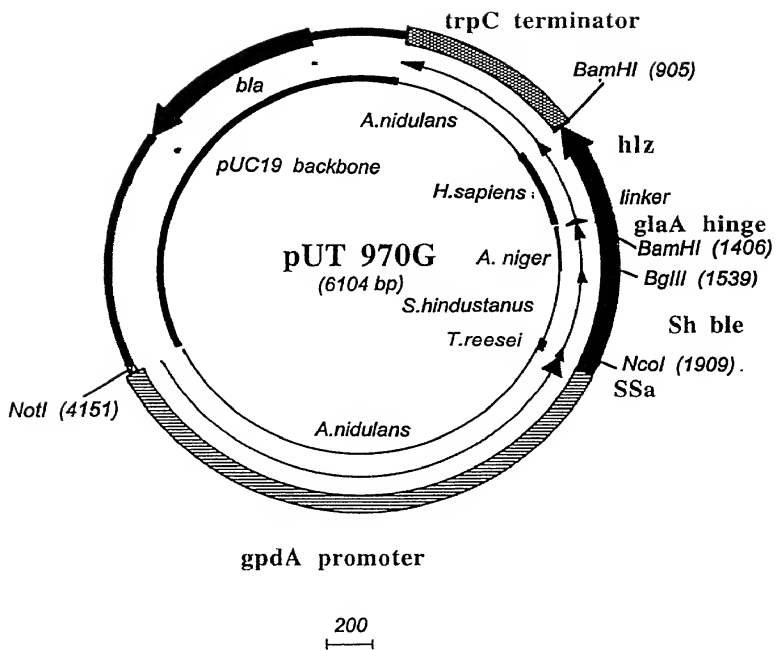
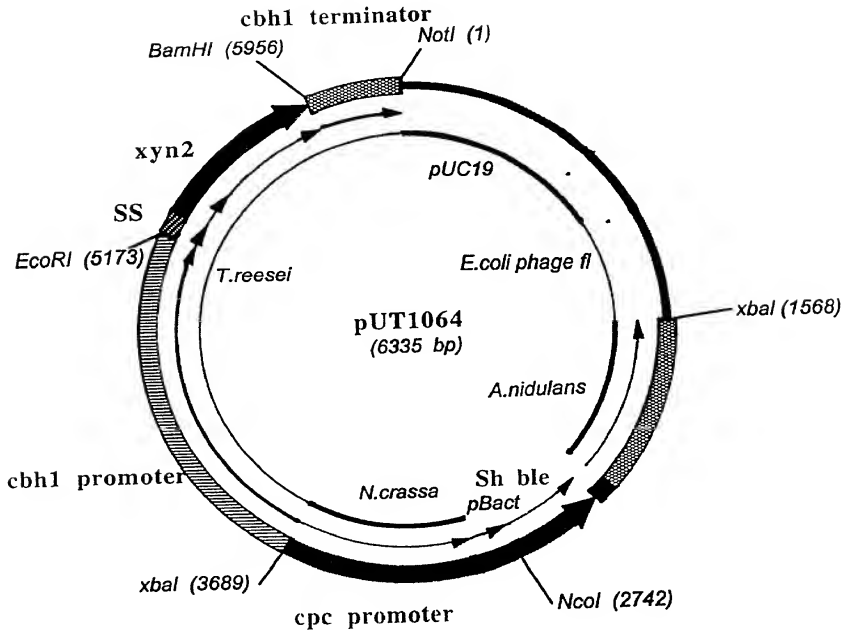
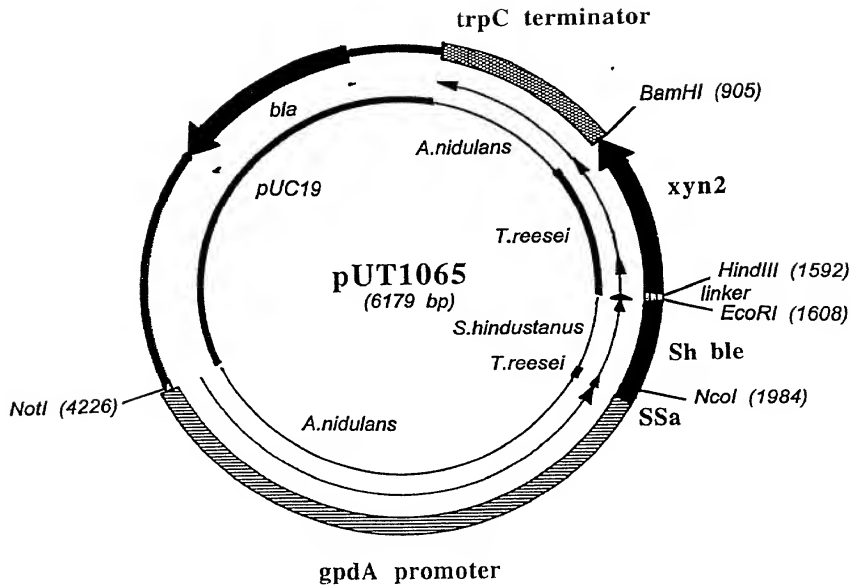


Fig 4



200

Fig 5



200

Fig 6

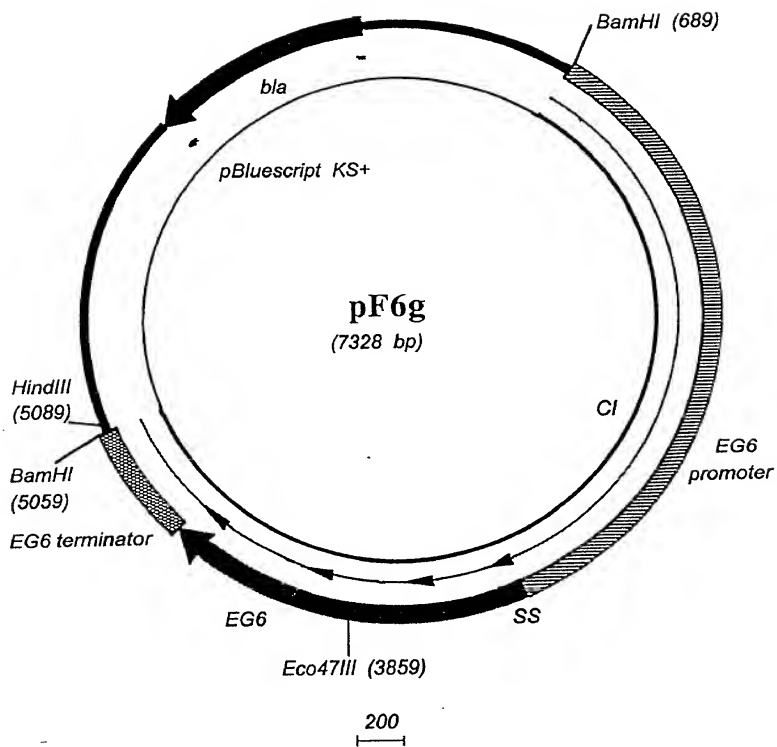
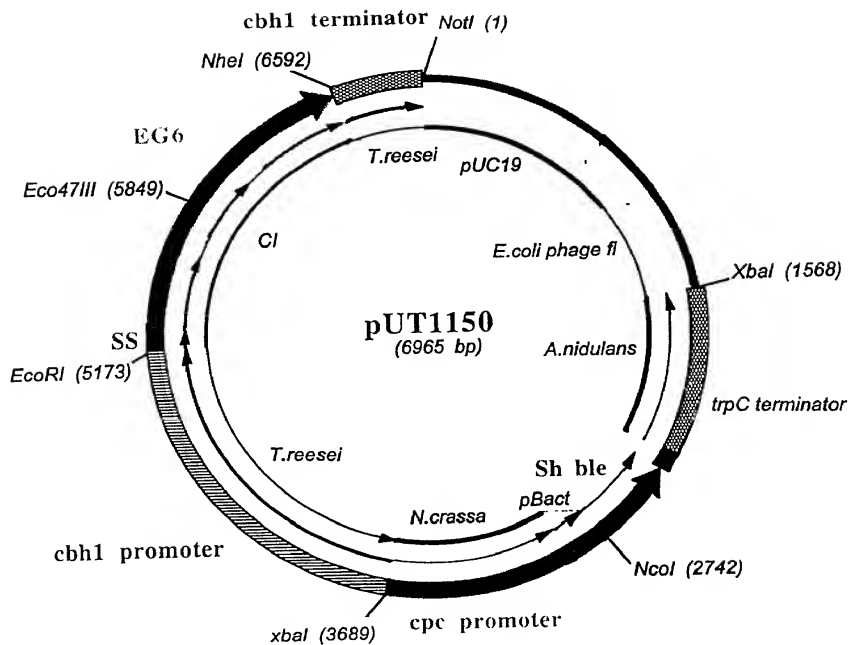


Fig 7



200

Fig 8

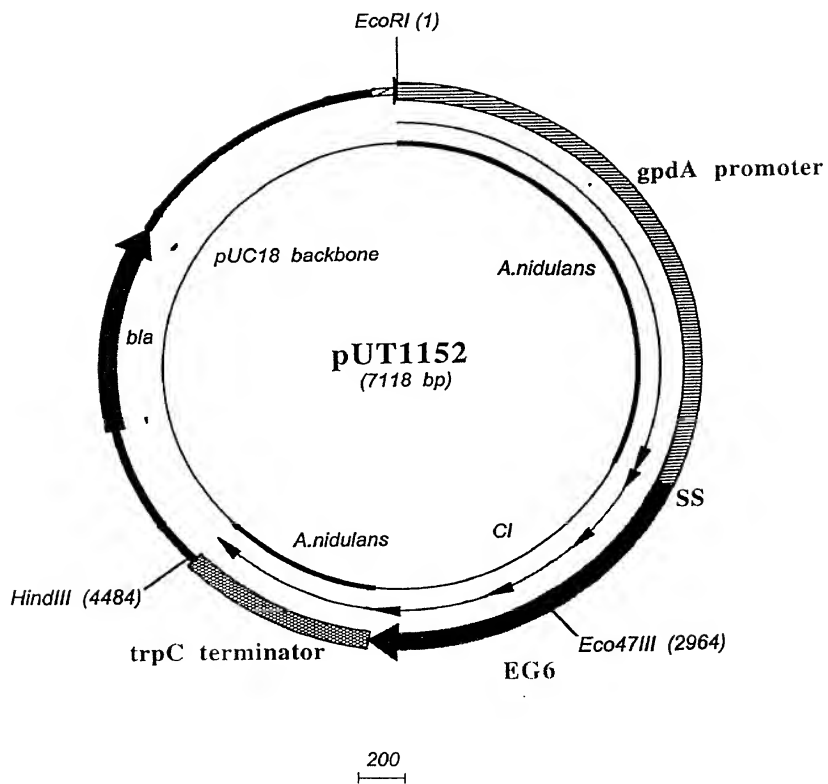
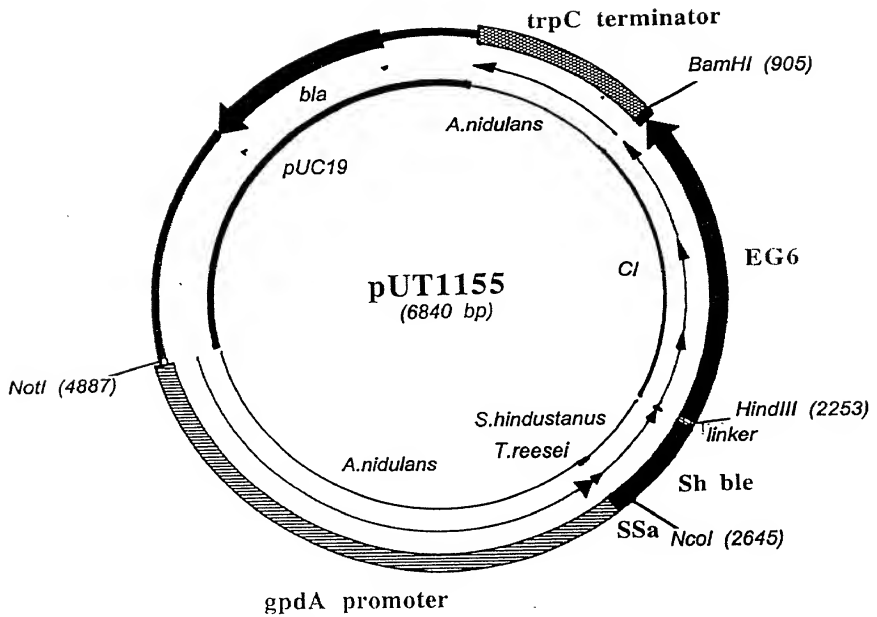


Fig 9



200

Fig 10

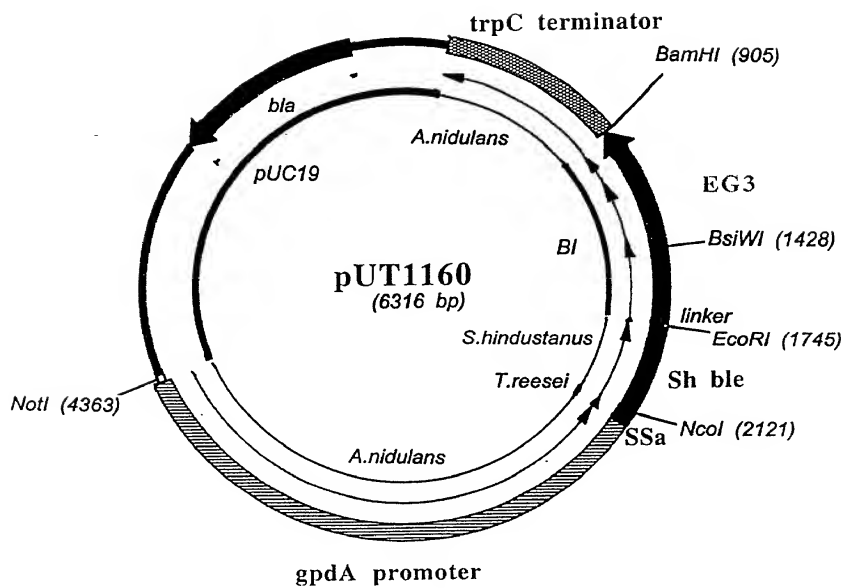
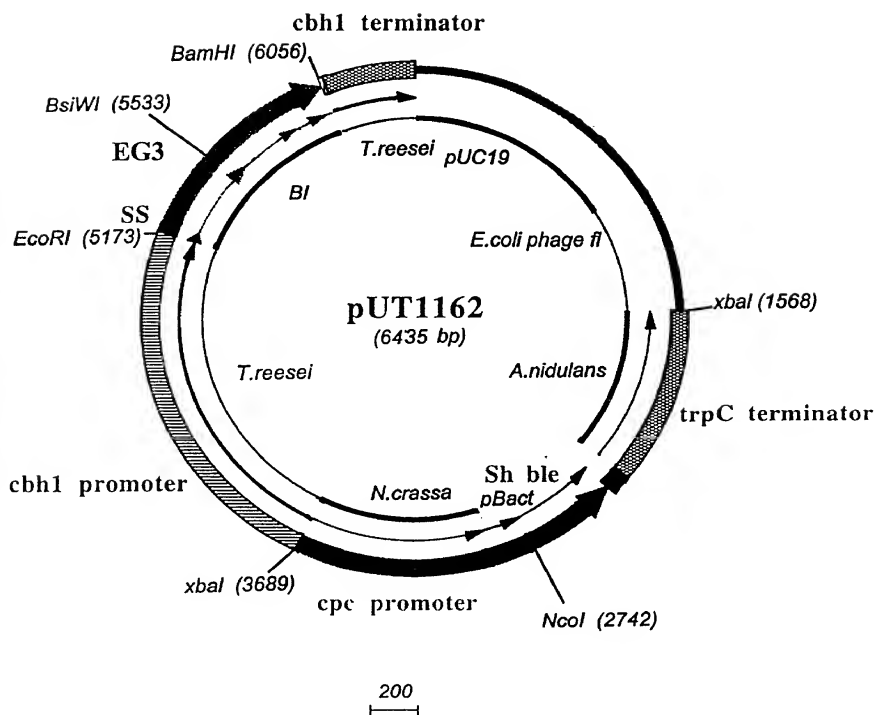


Fig 11



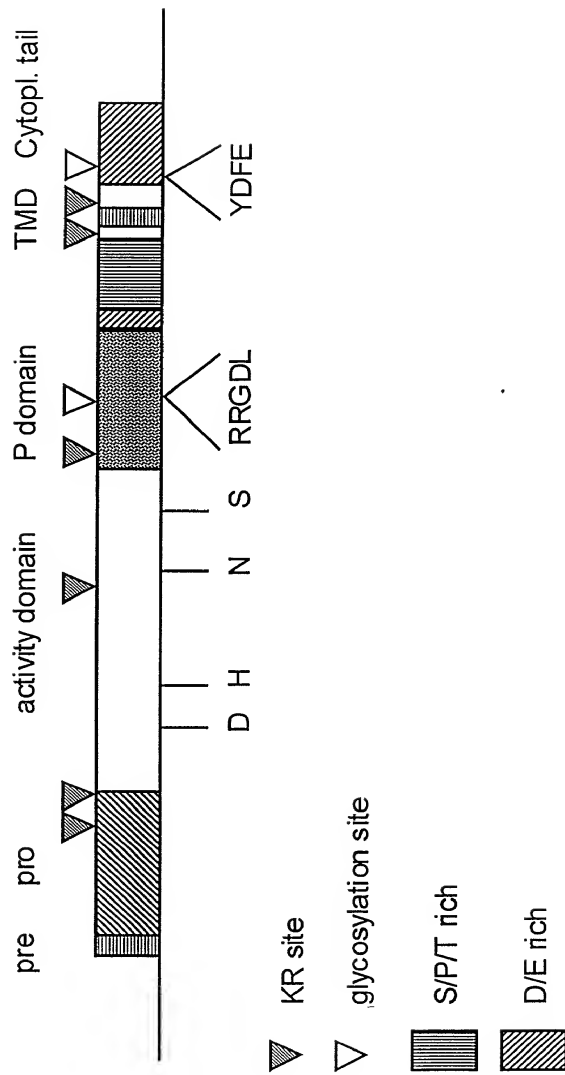


Fig 12

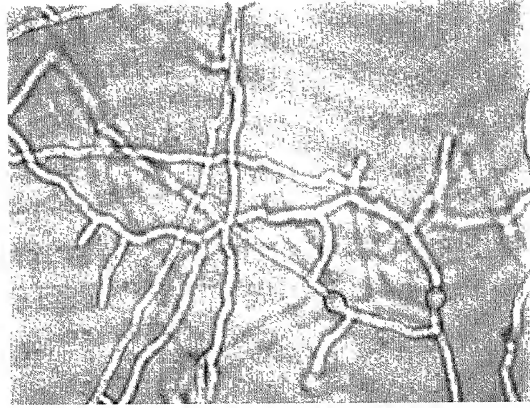


Fig 13A

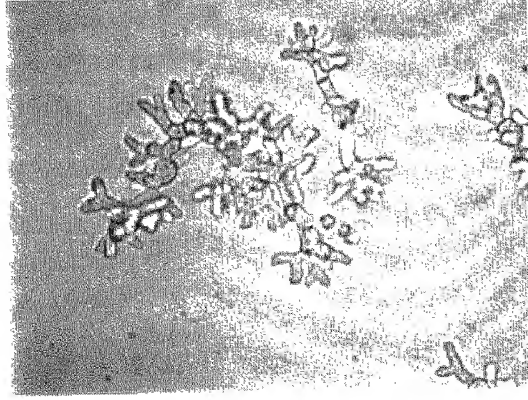


Fig 13B

100
90
80
70
60
50
40
30
20
10
0

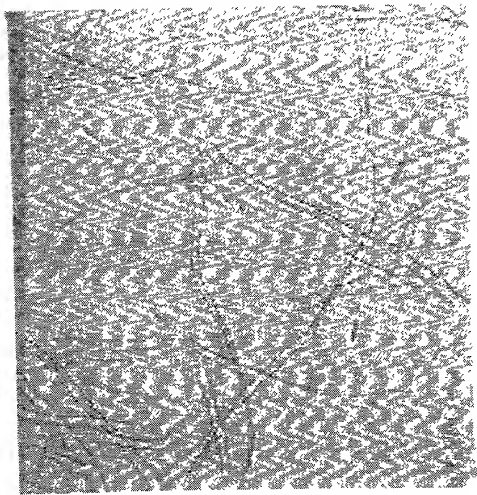


Fig. 14A

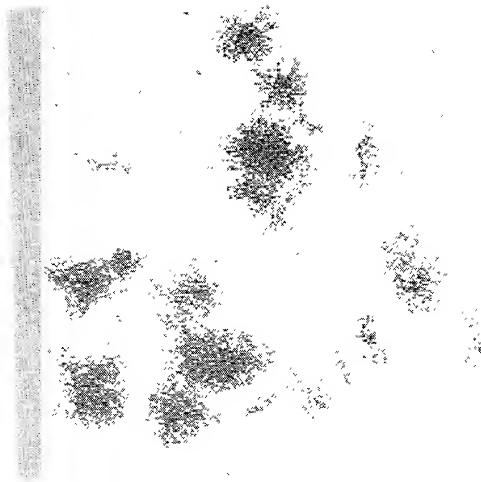


Fig. 14B

pyrE gene sequence

SEQ ID NO:1

Pyre/niger Length: 1578 March 9, 2001 09:28 Type: N Check: 2282

1 GGGTTAATGT GAAGGCGTTA GTGGTAATGT ATATTAATGG TGAGATGGC
51 TTTGATTGGG TTTAATTGGA ATCTGTATAT TTTCAGATGG AGTCAACTTT
101 TGAATGGCCA ATATATCCTC GGCGATACCG TCGGAGATAA GATAAGAATA
151 ATCGCACACT ATTCCCAAAG CATACTGGTA CATACTGCAT TCGGCTAGTG
201 CGGGGTGCTT ACCTCATCCA CCCGAATGAG CCCAACTTTT TTGTCTCAAT
251 CAATAATTGC ATCCAAATTC CCCCAGCACT TCCCCCTCCA ACCCCGTGTC
301 TATACCACTC CCTCCACACC CACACAATCA CAATGGCTCT CCCTGCCTAC
351 AAGACCGCCT TCCTGGAGTC TCTCGTCGGC CAACGTGCTG ACTTTCGGCA
401 CCTTCACCTT GAAGTCGGGT CGCCGTGCGT CACCCCTCCA ACACCGGCAT
451 TATCGCAATC GGAAGACTTA CCACTGTATA CAGACTCCCC CTACTTCTTC
501 AACGCCGGCA TCTTCAACAC CGCCTCTCTC CTCTCCGCC TCTCCACCAT
551 GGCCACACACC ATCATCACCT TCCTCGCTGA GAACCTTTC ATCCCCAAGC
601 CCGACGTCAT GCTTCGGGTA AAAAACCCCC TCTTTCCCCA ATACCCCACT
651 TCCACTCAAC AACCATAAA TAACTAACA AAACCCCTTA AACAGCCCCG
701 CATACAAAG CATCCCCCTC GCGTGCGCCA CCCTCCTTGA ACTCAACCGC
751 ATCGACCCCG CCACCTGGGG CAGCGTGTCC TACAGCTACA ACCGCAAAGA
801 AGCCAAGGAT CACGGCGAAG GCGGCAACAT TGTGCGCGCC GCTCTGAAGG
851 GCAAGACCGT GCTTGTGATC GACGATGTCA TCACGGCCGG TACCGCCATG
901 CGTGAGACCC TCAACCTGGT CGCCAAGGAG GCGCGCAAGG TCGTGGGATT
951 CACTGTGTCT CTGACCGCT TGGAGAAGAT GCCCGGACCC AAGGACGAGA
1001 ACGGTGTCGA GGACGATAAG CCCAGAATGA GTGCTATGGG TCAGATCCGT
1051 AAGGAGTATG GTGTGCCAC GACGAGTATT GTTACTCTGG ATGATTTGAT
1101 CAAGTTGATG CAGGCGAAGG GCAATGAGGC CGATATGAAG CGGTTGGAGG
1151 AGTATAGGGC TAAGTATCAG GCTAGTGATT AGTCGGTTTC ATTGACCGAT

FIG. 15A

1201 TGTTTGGGTG GGTGTGAGAG GTTAGGTTAG GTTGTGGGCG TAGGAATGAA
 1251 AAGCTGTATA CATAGGGGCC TGAAGAGGTG CGTAGAGACG GTCGTGAGAT
 1301 GTTTTATGTC AAAATCTTGA ACAAATGACA CCTTAAAAAA GACCCCTTGG
 1351 TTTCAGCTGA ATTAGCCCGG AAAGATGCTC GGCACGCCAT GAGTCTAGCC
 1401 CACTCAGTGG GCACCCGTTT CCCACATTTG AAGTGGCCGA CGCTTATTTG
 1451 GCTGAGGCTG TGGCCTGGAA AGGCACTATG GCGTGCTGCG GTACAAGGCC
 1501 GGGGTGCGG TACGAACCAC GACGCCCCGAA GGGAACTCTT CGGTCTTACT
 1551 ACTACTATGT CCCCAGTTGA CCCCCGA

SEQ ID NO:2

Translation of pyrE(1-1578)
 Universal code

1 GGGTTAATGTGAAGGCGTTAGTGGTAATGTATATTAAATGGTGAGATGGGCTTGTATTGGG
 CCCAATTACACTTCGCAATCACCATTACATATAATTACCACTCTACCCGAAACTAACCC
 1 G L M * R R * W * C I L M V R W A L I G
 1 G * C E G V S G N V Y * W * D G L * L G
 1 V N V K A L V V M Y I N G E M G F D W V
 61 TTTAATTGGAATCTGTATATTTTCAGATGGAGTCAACTTTTGAATGGCCAATATATCCTC
 AAATTAACCTTAGACATATAAAAGTCTACCTCAGTTGAAAACCTACCGGTTATATAGGAG
 21 F N W N L Y I F R W S Q L L N G Q Y I L
 21 L I G I C I F S D G V N F * M A N I S S
 21 * L E S V Y F Q M E S T F E W P I Y P R
 121 GCGGATACCGTCGGAGATAAGATAAGAATAATCGCACACTATTCCCAAAGCATACTGGTA
 CCGCTATGGCAGCCTCTATTCTATTCTTATTAGCGTGTGATAAGGGTTTCGTATGACCAT
 41 G D T V G D K I R I I A H Y S Q S I L V
 41 A I P S E I R * E * S H T I P K A Y W Y
 41 R Y R R R * D K N N R T L F P K H T G T
 181 CATACTGCATTGCGCTAGTGCGGGGTGCTTACCTCATCCACCCGAATGAGCCCACTTTT
 GTATGACGTAAGCCGATCACGCCCCACGAATGGAGTAGGTGGGCTTACTCGGGTTGAAAA
 61 H T A F G * C G V L T S S T R M S P T F
 61 I L H S A S A G C L P H P P E * A Q L F
 61 Y C I R L V R G A Y L I H P N E P N F F

FIG. 15B

241 TTGTCTCAATCAATAATTGCATCCAAATTCCCCCGCAACTTCCCCCTCCAACCCCGTGT
AACAGAGTTAGTTATTAACGTAGGTTTAAGGGGGCGTTGAAGGGGGAGGTTGGGCACAG

81 L S Q S I I A S K F P R N F P L Q P R V
81 C L N Q * L H P N S P A T S P S N P V S
81 V S I N N C I Q I P P Q L P P P T P C L
?????????

301 TATACCACTCCCTCCACACCCACACAATCACAATGGCTCTCCCTGCCTACAAGACCGCT
ATATGGTGAGGGAGGTGTGGGTGTGTAGTGTTACCGAGAGGGACGGATGTTCTGGCGGA

101 Y T T P S T P T Q S Q W L S L P T R P P
101 I P L P P H P H N H N G S P C L Q D R L
101 Y H S L H T H T I T M A L P A Y K T A F

361 TCCTGGAGTCTCTCGTCGGCCAACGTGCTGACTTTCCGGCACCTTCACCCTGAAGTCGGGT
AGGACCTCAGAGAGCAGCCGTTGCACGACTGAAAGCCGTGGAAGTGGGACTTCAGCCCA
????????????????????

121 S W S L S S A N V L T F G T F T L K S G
121 P G V S R R P T C * L S A P S P * S R V
121 L E S L V G Q R A D F R H L H P E V G S

INTRON I

421 CGCCGTGCGTCAACCCCTCCAAACACCGGCATTATCGCAATCGGAAGACTTACCCTGTATA
CGGCGACGCAGTGGGGAGGTTGTGGCCGTAATAGCGTTAGCCTTCTGAATGGTGACATAT

141 R R A S P L Q H R H Y R N R K T Y H C I
141 A V R H P S N T G I I A I G R L T T V Y
141 P C V T P P T P A L S Q S E D L P L Y T

481 CAGACTCCCCCTACTTCTTCAACGCCGCATCTTCAACACCGCCTCTCTCCTCTCGGCC
GTCTGAGGGGGATGAAGAAGTTGCGGCCGTAGAAGTTGTGGCGGAGAGAGAGAGGCGGG

161 Q T P P T S S T P A S S T P P L S S P P
161 R L P L L L Q R R H L Q H R L S P L R P
161 D S P Y F F N A G I F N T A S L L S A L

NcoI

541 TCTCCACCATGGCCCACACCATCATCACCTTCTCGCTGAGAACCCTTCCATCCCCAAGC
AGAGGTGGTACCGGGGTGTGTAGTAGTGAAGGAGCGACTCTTGGGAGGTAGGGGTTCG

181 S P P W P T P S S P S S L R T L P S P S
181 L H H G P H H H L P R * E P F H P Q A
181 S T M A H T I I T F L A E N P S I P K P
???????????? INTRON II

601 CCGACGTATGCTTCGGGTAAAAAACCCCTCTTTCCCAATACCCCACTTCCACTCAAC
GGTGTCAGTACGAAGCCCATTTTTGGGGGAGAAAGGGTTATGGGGTGAAGGTGAGTTG

201 P T S C F G * K T P S F P N T P L P L N
201 R R H A S G K K P P L S P I P H F H S T
201 D V M L R V K N P L F P Q Y P T S T Q Q

FIG. 15C

661 AACCCATAAATAACTAACAAAAACCCCTAAACAGCCCCGCATACAAAGGCATCCCCCTC
TTGGGTATTTATTGATTGTTTTTGGGGGATTGTCTGGGGCGTATGTTTCCGTAGGGGGAG

221 N P * I T N K N P L N S P A Y K G I P L
221 T H K * L T K T P * T A P H T K A S P S
221 P I N N * Q K P P K Q P R I Q R H P P R

721 GCGTGCGCCACCTCCTTGAACCTCAACCGCATCGACCCCGCCACCTGGGGCAGCGTGTCC
CGCAGCGCGTGGGAGGAACCTTGAGTTGGCGTAGCTGGGGCGGTGGACCCCGTCGCACAGG

241 A C A T L L E L N R I D P A T W G S V S
241 R A P P S L N S T A S T P P P G A A C P
241 V R H P P * T Q P H R P R H L G Q R V L

781 TACAGCTACAACCGCAAGAAGCCAAAGGATCACGGCGAAGGCGGCAACATTGTCTGGCGCC
ATGTCGATGTTGGCGTTTCTTCGGTTCCTAGTGCCGCTTCCGCCGTTGTAACAGCCGCGG

261 Y S Y N R K E A K D H G E G G N I V G A
261 T A T T A K K P R I T A K A A T L S P P
261 Q L Q P Q R S Q G S R R R R Q H C R R R

841 *KpnI*
GCTCTGAAGGGCAAGACCGTGCTTGTGATCGACGATGTCATCACGGCCGGTACCGCCATG
CGAGACTTCCCGTTCTGGCACGAACTAGCTGCTACAGTAGTGCCGGCCATGCGCGTAC

281 A L K G K T V L V I D D V I T A G T A M
281 L * R A R P C L * S T M S I R P V P M C
281 S E G Q D R A C D R R C H H G R Y R H A

901 CGTGAGACCCCTCAACCTGGTCGCCAAGGAGGGCGGCAAGGTCGTGCGGATTCACCTGTTGCT
GCACTCTGGGAGTTGGACCAGCGGTTCTCCGCCGTTCCAGCAGCCTAAGTGACAACGA

301 R E T L N L V A K E G G K V V G F T V A
301 V R P S T W S P R R A A R S S D S L L L
301 * D P Q P G R Q G G R Q G R R I H C C S

961 CTGGACCGCTTGGAGAAGATGCCCGGACCCAAGGACGAGAACGGTGTGAGGACGATAAG
GACCTGGCGAACCTCTTCTACGGGCTGGGTTCTGCTCTTGCCACAGCTCCTGCTATTCT

321 L D R L E K M P G P K D E N G V E D D K
321 W T A W R R C P D P R T R T V S R T I S
321 G P L G E D A R T Q G R E R C R G R * A

1021 CCCAGAATGAGTGCTATGGGTCAGATCCGTAAGGAGTATGGTGTGCCACGACGAGTATT
GGGTCTTACTCACGATACCCAGTCTAGGCATTCCTCATACCACACGGGTGCTGCTCATAA

341 P R M S A M G Q I R K E Y G V P T T S I
341 P E * V L W V R S V R S M V C P R R V L
341 Q N E C Y G S D P * G V W C A H D E Y C

FIG. 15D

1081 GTTACTCTGGATGATTGATCAAGTTGATGCAGGCGAAGGGCAATGAGGCCGATATGAAG
CAATGAGACCTACTAACTAGTTCAACTACGTCCGCTTCCCGTTACTCCGGCTATACTTC

361 V T L D D L I K L M Q A K G N E A D M K
361 L L W M I * S S * C R R R A M R P I * S
361 Y S G * F D Q V D A G E G Q * G R Y E A

1141 CGGTTGGAGGAGTATAGGGCTAAGTATCAGGCTAGTGATTAGTCGGTTTCATTGACCGAT
GCCAACCTCCTCATATCCCGATTATAGTCCGATCACTAATCAGCCAAAGTAAC TGGCTA

381 R L E E Y R A K Y Q A S D * S V S L T D
381 G W R S I G L S I R L V I S R F H * P I
381 V G G V * G * V S G * * L V G F I D R L

1201 TGTTTGGGTGGGTGTGAGAGGTTAGGTTAGGTTGTGGGCGTAGGAATGAAAAGCTGTATA
ACAAACCCACCCCACTCTCCAATCCAATCCAACACCCGCATCCTTACTTTTCGACATAT

401 C L G G C E R L G * V V G V G M K S C I
401 V W V G V R G * V R L W A * E * K A V Y
401 F G W V * E V R L G C G R R N E K L Y T

1261 CATAGGGGCCTGAAGAGGTGCGTAGAGACGGTCGTGAGATGTTTTATGTCAAAATCTTGA
GTATCCCGGACTTCTCCACGCATCTCTGCCAGCACTTACAAAATACAGTTT TAGAACT

421 H R G L K R C V E T V V R C F M S K S *
421 I G A * R G A * R R S * D V L C Q N K L E
421 * G P E E V R R D G R E M F Y V K I L N

1321 ACAAATGACACCTTAAAAAGACCCCTTGGTTTCAGCTGAATTAGCCCGGAAAGATGCTC
TGTTTACTGTGGAATTTTTTCTGGGGAACCAAAGTCGACTTAATCGGGCCTTTGTACGAG

441 T N D T L K K T P W F Q L N * P G K M L
441 Q M T P * K R P L G F S * I S P E R C S
441 K * H L K K D P L V S A E L A R K D A R

1381 GGCACGCCATGAGTCTAGCCCACTCAGTGGGCACCCGTTTCCACATTTGAAGTGGCCGA
CCGTGCGGTACTCAGATCGGTGAGTCACCCGTGGGCAAAGGTGTAAACTTCACCGGCT

461 G T P * V * P T Q W A P V S H I * S G R
461 A R H E S S P L S G H P F P T F E V A D
461 H A M S L A H S V G T R F P H L K W P T

1441 CGCTTATTTTGGCTGAGGCTGTGGCCTGGAAGGCACATATGGCGTGCTGCGGTACAAGGCC
GCGAATAAACCGACTCCGACACCGGACCTTTCGTGATACCGCACGACGCCATGTTCCGG

481 R L F G * G C G L E R H Y G V L R Y K A
481 A Y L A E A V A W K G T M A C C G T R P
481 L I W L R L W P G K A L W R A A V Q G R

FIG. 15E

